

1 tcttctaccatctgctccccagagggtgctgctgtgcacttgggtcctggagcccttctccaccggatagattctcacccttggcccgctttg
 101 cccacccctactctgcccagaagtgcagagcctaagccgcctccatggccccaggaaggattcaggggagaggcccaaacaggagccacgcagcca
 -20 -10
 MetGluLeuThrGluLeuLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp
 201 gacacccccggcagaATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCTCTCTGTTG
 10 20 30 40
 LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
 301 ACCTCCGAGTCTCAGTAAACTGCTTCGTGACTCCCATGTCTTACAGCAGACTGAGCCAGTCCCCAGAGGTTACCCCTTTGCCCTACACCTGTCTCTGT
 50 60 70
 ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
 401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCTTCTGCTGGAGGGAGTG
 80 90 100
 MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
 501 ATGGCAGCAGGGGACAACCTGGGACCCACTTGCCTCTCATCCCTCTCTGGGCGAGCTTCTGGACAGGTCCGCTCTCTCTCTGGGCCCTGCAGAGCCCTC
 110 120 130 140
 GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
 601 TTGGAACCCAGCTTCTCCACAGGGCAGGACACAGCTCACAAGGATCCCAATGCCATCTTCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCTTT
 150 160 170
 LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu
 701 CCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACACAGCTGTCCCCAGCAGAACCTCTCTAGTCTCACAACGAGCTC
 180 190 200
 ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle
 801 CCAAACAGGACTTCTGGATTGTGGAGACAAACTTCACTGCCTCAGCCAGAAGTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGATTTCAGAGCCAAGA
 210 220 230 240
 ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro
 901 TTCCTGGTCTGCTGAACCAACCTCCAGGTCCCTGGACCAATCCCCGATACCTGAAACAGGATACACGAACCTTGAATGGAACCTCGTGACTCTTTCC
 250 260 270
 GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer
 1001 TGGACCCCTCAGCAGGACCCTAGGAGCCCCGACATTCTCTCAGGAACATCAGACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGATATTCTCTCTCC
 280 290 300
 ProThrHisProProThrGlyGlnTyrThrLeuPheProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla
 1101 CCAACCCATCTCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGGCCACCCCTGTGGTCCAGCTCCACCCCTGCTTCTGACCTTCTG
 310 320 330
 ProThrProThrProThrSerProLeuLeuAsnThrSerTyrThrHisSerGlnAsnLeuSerIleGluGly
 1201 CTCCAACGCCCAACCCCTACCAGCCCTCTTCTAAACACATCTACACCCACTCCCAAGATCTGTCTCAGGAAGGTAAGgttctcagacactgccgacatc
 1301 agcattgtctcatgtacagctcccttccctgcagggcgccctgggagacaactggacaagatttctactttctcctgaaacccaaagccctggtaaaa
 1401 gggatacacaggactgaaaagggaaatcatttttctactgtacattataaaccttcagaagctattttttaagctatcagcaatactcatcagagcagcta
 1501 gctcttttggctctattttctgcagaaatttgcaactcactgatttctctacatgctcttttctgtgataactctgcaaggcctgggctggcctggcagtt
 1601 gaacagagggagagactaaccttgagtcagaaaacagagaaagggttaatttcttctgcttcaaatcaaggccttccaacgccccatcccccttactat
 1701 cattctcagtgaggactctgatcccatattcttaacagatcttactcttgagaaatgaataagcttctctcagaaaaa

FIG. 1

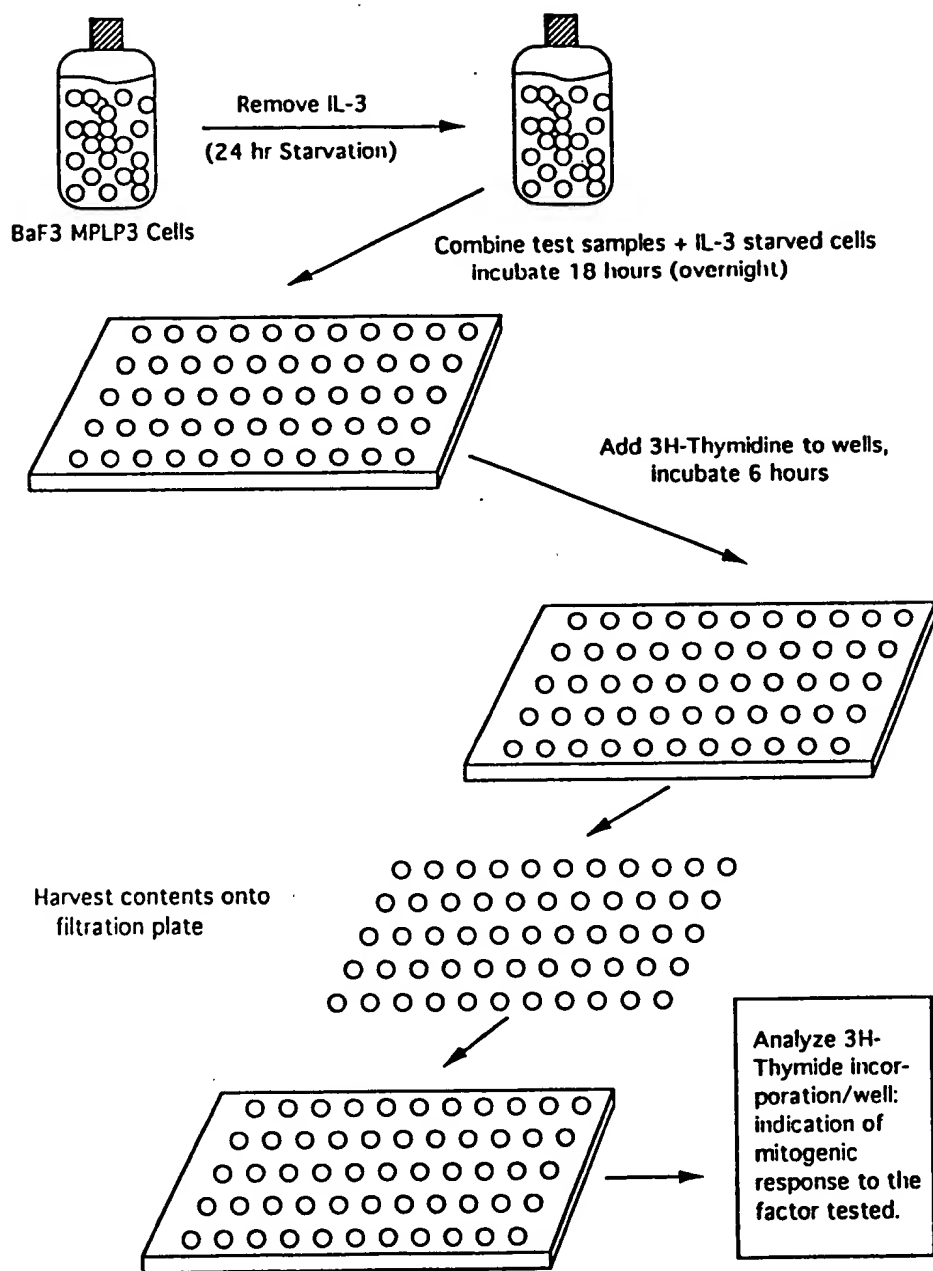


FIG. 2

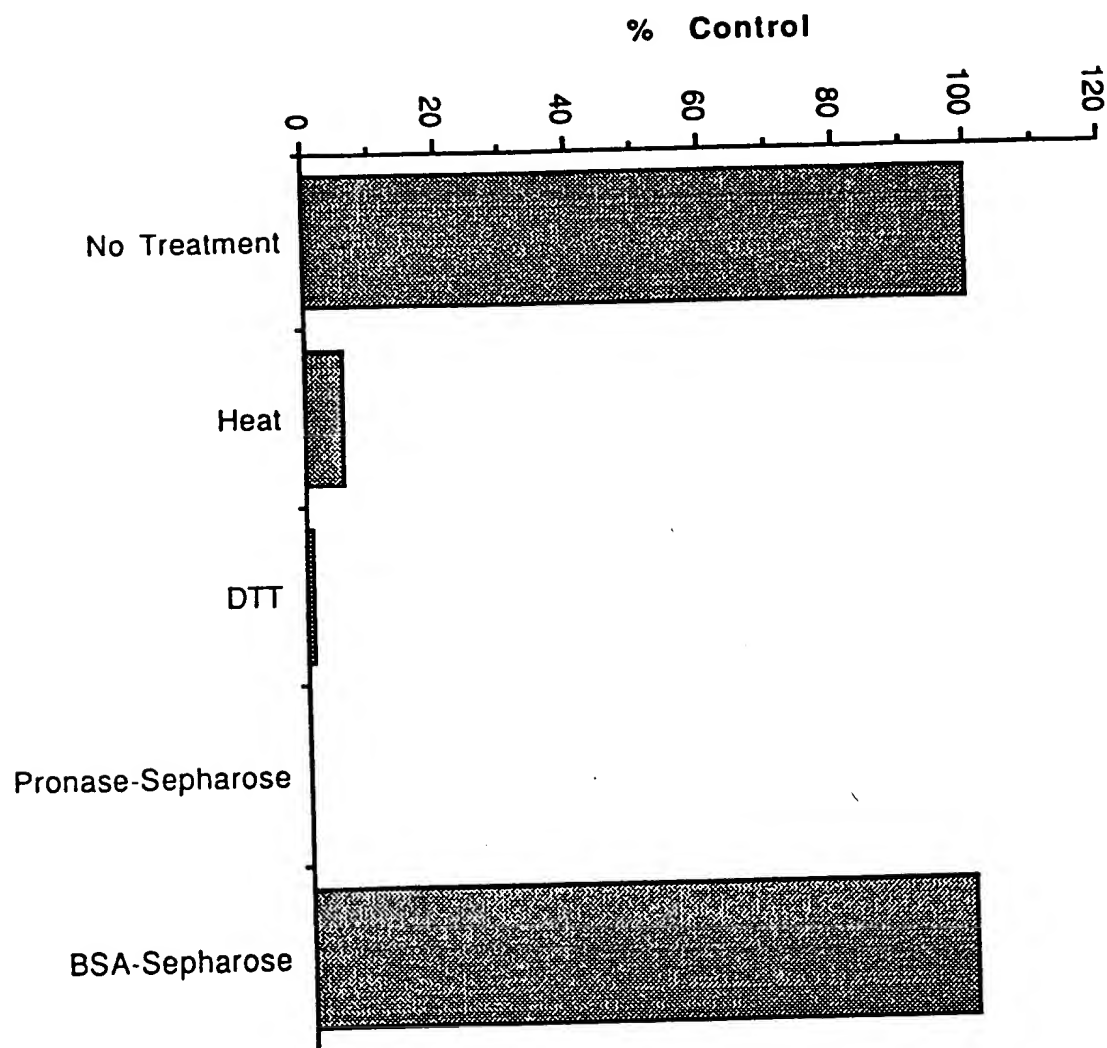


FIG. 3

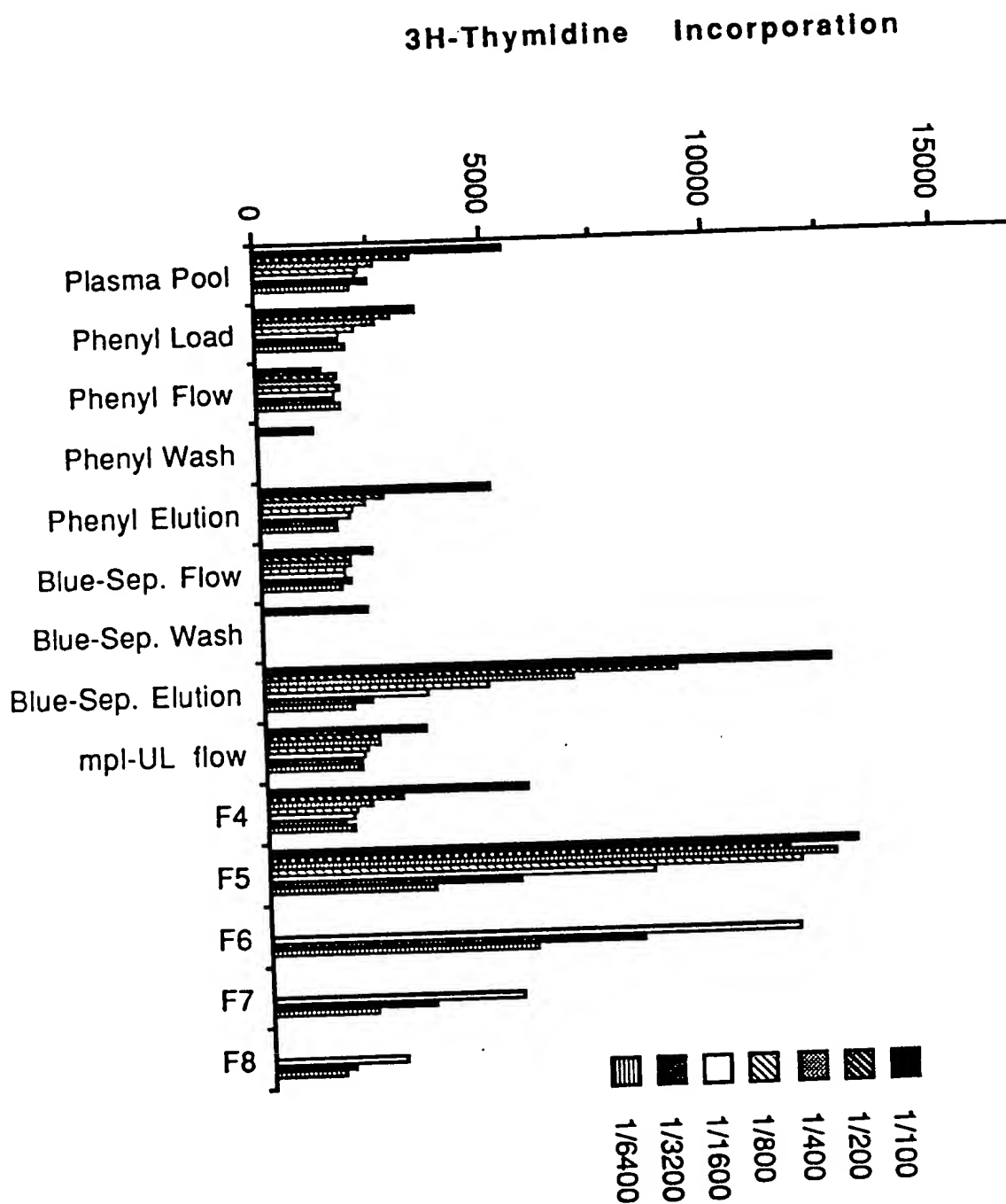


FIG. 4

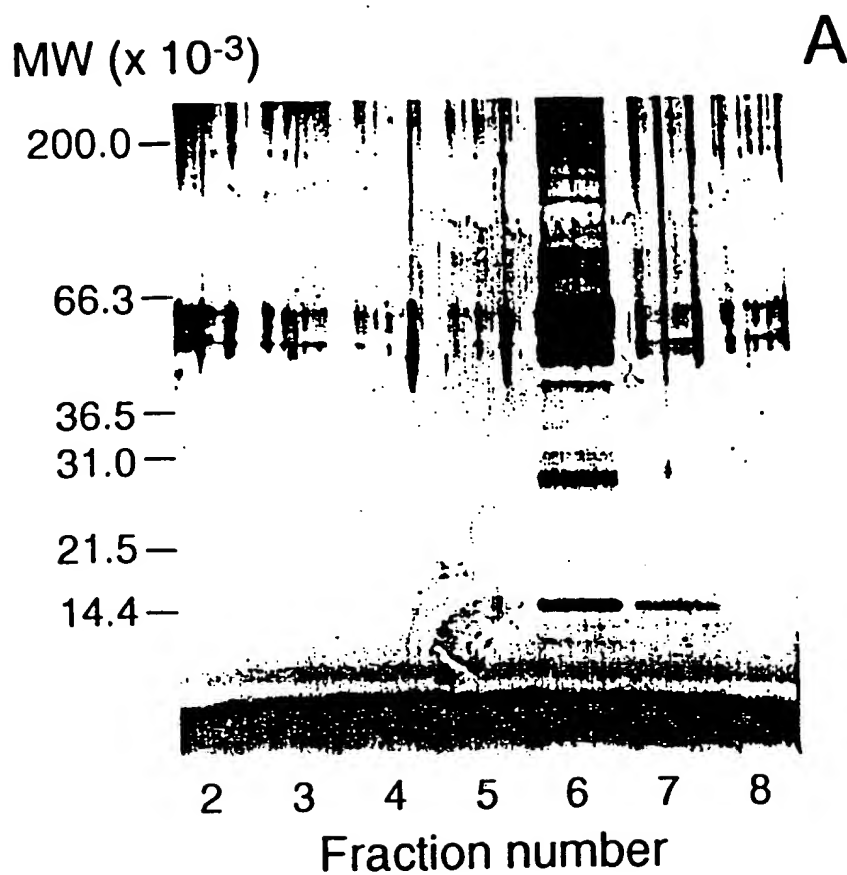


FIG. 5

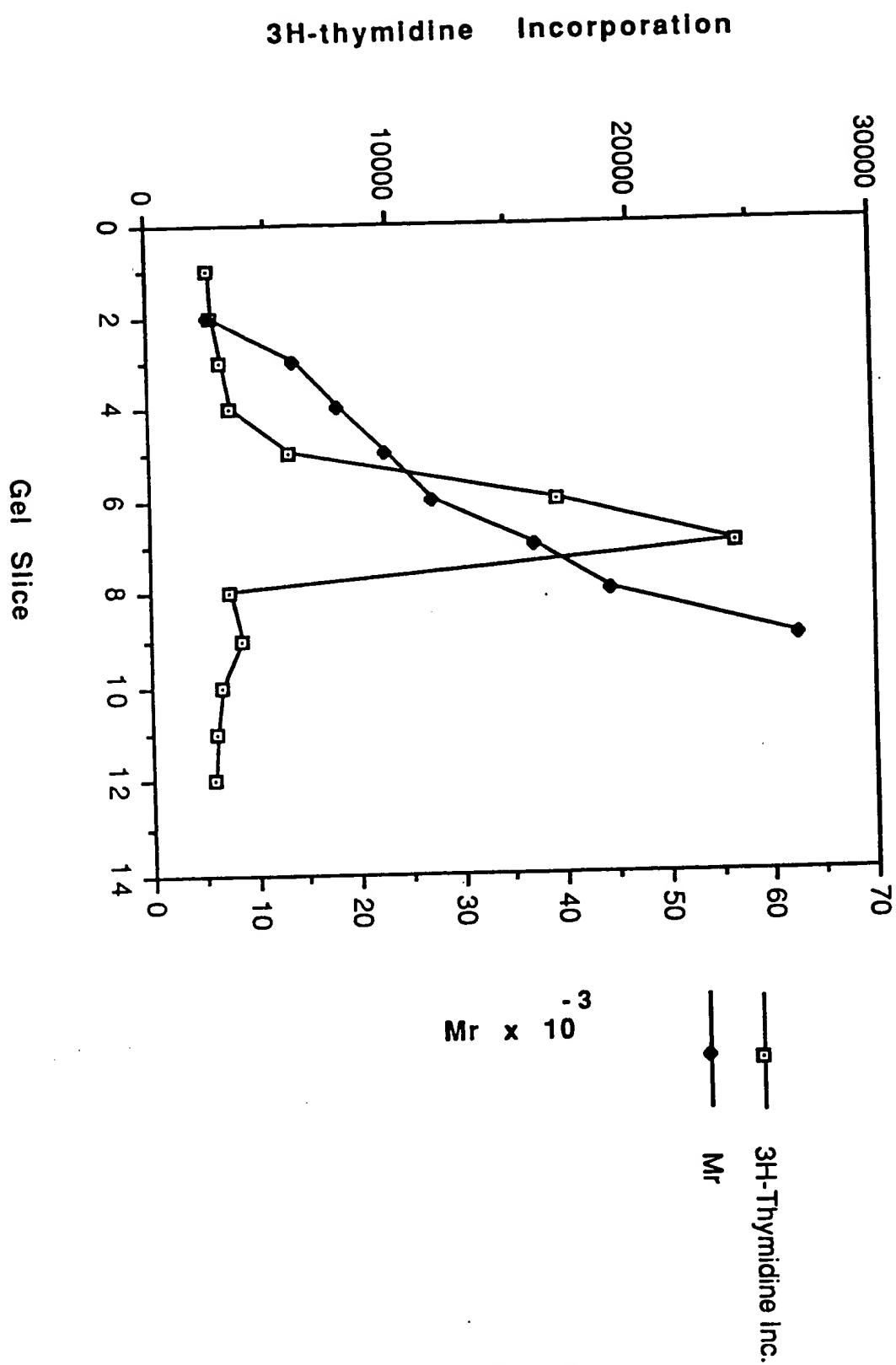


FIG. 6

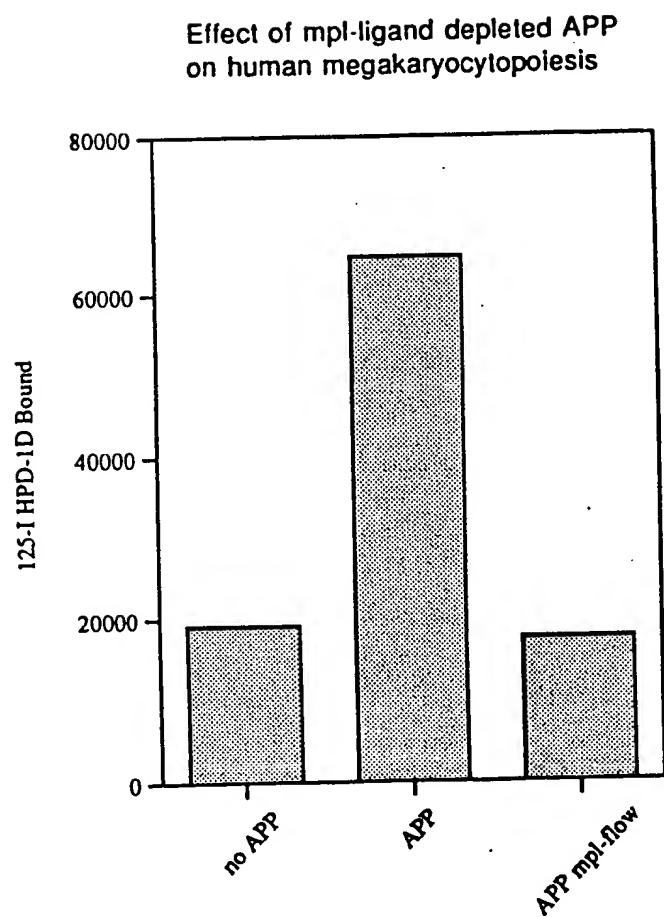


FIG. 7

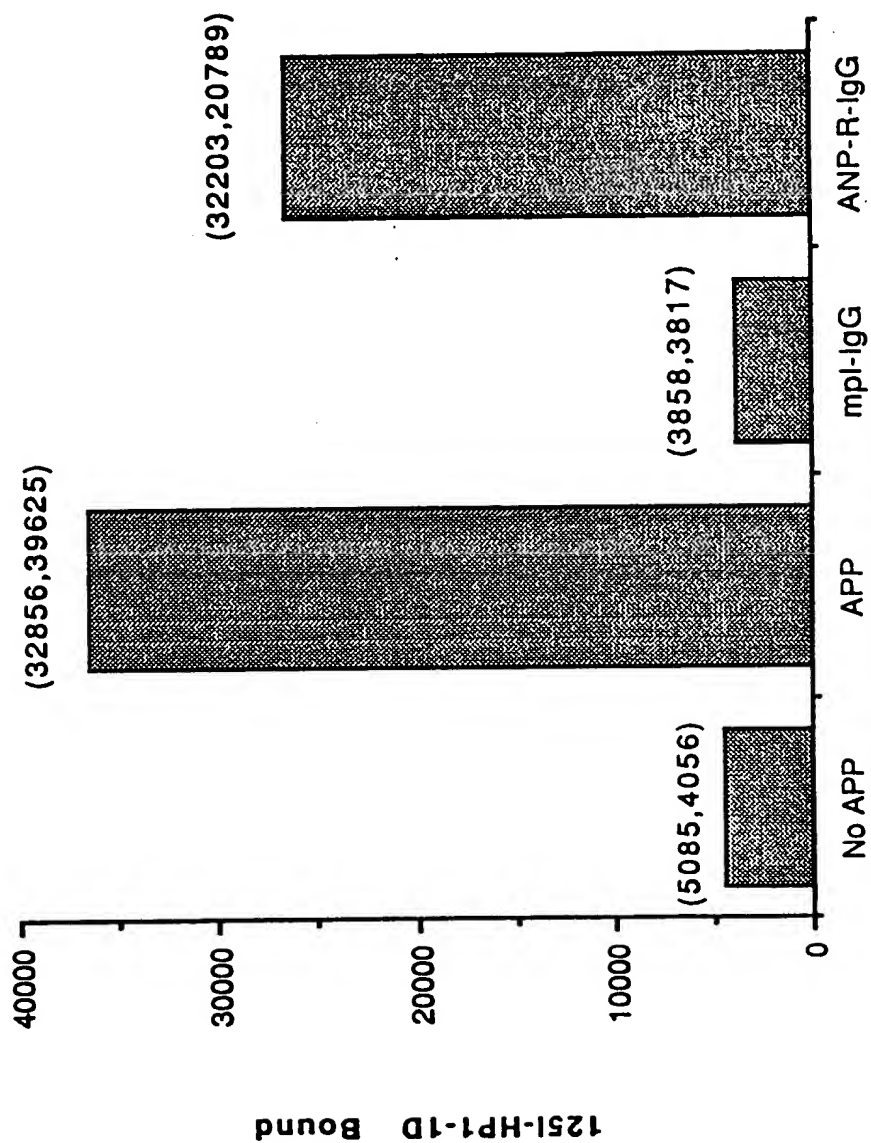


FIG. 8

-10
L L L V V M L L L T
↓

1 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT
CTTAAGGACC TTATGGTCCA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA

10
A R L T L S S P A P P A C D L R V L S K L L R D S H V L H S R L ↓

101 GCAAGGCTAA CGTGTCCAG CCCGGCTCCT CCTGCTTGAG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA
CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT

20

201 GAACTCCCAA CATTATCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA GACACCATCA CTTCTCTTAA CTCCTTGACC CAATGACTAT
CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACCTGG GTTACTGATA

30

301 TCTTCCCATTA TTGTCCCCAC CTAATGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT ACAGCCCCGA TTTAAAAGCT CTCGTCTAGA
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA AGAAGTGTTA TGTCGGGCGT AAATTTTGA GAGCAGATCT

FIG. 9

h-ML	1	S	P	A	P	P	A	C	D	L	R	V	L	S	K	L	R	D	S	H	V	L	H	S	R	L	S	Q	C	P	E	V	H	P	L	P	T	P	V	L	L	P	A	V	D	F	S	L	G	E	
h-epo	1	A	P	P	R	L	I	C	D	S	R	V	L	E	R	V	L	L	E	A	K	E	A	E	N	I	T	T	G	C	A	E	H	C	S	L	N	E	N	I	T	V	P	D	T	K	V	N	F	Y	A
h-ML	51	W	K	I	T	O	M	E	E	T	K	A	Q	D	I	L	G	A	V	T	L	L	E	G	V	M	A	A	R	G	Q	L	G	P	T	C	L	S	-	-	S	L	L	G	Q	L	S	G	Q	V	R
h-epo	51	W	K	R	M	E	V	G	Q	Q	A	V	E	V	M	Q	G	L	A	L	L	S	E	A	V	L	R	G	O	A	L	L	V	N	S	S	O	P	W	E	P	L	Q	L	H	V	D	K	A	V	S
h-ML	99	L	L	-	-	L	G	A	L	O	S	L	L	G	T	Q	-	-	L	P	P	Q	G	R	T	T	A	H	K	D	P	N	A	I	F	L	S	F	O	H	L	L	R	G	K	V	R	F	L		
h-epo	101	G	L	R	S	L	T	T	L	R	A	L	G	A	O	K	E	A	I	S	P	P	D	A	A	S	A	A	P	L	R	T	I	T	A	D	T	F	R	K	L	L	F	R	I	V	S	N	F	L	R
h-ML	143	-	-	M	L	V	G	G	S	T	L	C	V	R	R	A	P	P	T	T	A	V	P	S	R	T	S	L	V	L	T	L	N	E	L	P	N	R	T	S	G	L	L	E	T	N	F	T	A	S	
h-epo	151	G	K	L	K	L	Y	T	G	E	A	C	R	T	G	D	R																																		
h-ML	191	R	T	T	G	S	G	L	L	K	W	Q	Q	G	F	R	A	K	I	P	G	L	L	N	O	T	S	R	S	L	D	O	I	P	G	Y	L	N	R	I	H	E	L	L	N	G	T	R	G	L	F
h-ML	241	P	G	P	S	R	R	T	L	G	A	P	D	I	S	S	G	T	S	D	T	G	S	L	P	P	N	L	O	P	G	Y	S	P	S	P	T	H	P	P	T	G	O	Y	T	L	F	P	L	P	P
h-ML	291	T	L	P	T	P	V	V	O	L	H	P	L	L	P	D	P	S	A	P	T	P	T	P	S	P	L	L	N	T	S	Y	T	H	S	Q	N	L	S	O	E	G									

FIG. 10

hML	1	SPAPPACDLRVLSKLLRDSHVLHSRLSQCPVHPLPTPVLLPAVDFSLGE
hML2	1	SPAPPACDLRVLSKLLRDSHVLHSRLSQCPVHPLPTPVLLPAVDFSLGE
hML3	1	SPAPPACDLRVLSKLLRDSHVLHSRLSQCPVHPLPTPVLLPAVDFSLGE
hML4	1	SPAPPACDLRVLSKLLRDSHVLHSRLSQCPVHPLPTPVLLPAVDFSLGE
hML	51	WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML2	51	WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML3	51	WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML4	51	WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML	101	LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML2	101	LGALQSLLGT- - - QGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML3	101	LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGK- DFW- IVGDKLH
hML4	101	LGALQSLLGT- - - QGRTTAHKDPNAIFLSFQHLLRGK- DFW- IVGDKLH
hML	151	CVRRAPPTTAVPSRTSLVLTNLNLPNRTSGLLETNFTASARTTGSGLLKW
hML2	147	CVRRAPPTTAVPSRTSLVLTNLNLPNRTSGLLETNFTASARTTGSGLLKW
hML3	149	CLSQ- - - - - NYWL- - - - - WAS- - - - - SEVAAGIQSQDSWSAEPNLQ- -
hML4	145	CLSQ- - - - - NYWL- - - - - WAS- - - - - SEVAAGIQSQDSWSAEPNLQ- -
hML	201	QGGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML2	197	QGGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML3	179	VP- - - - - E- - - - - QDTRTLEWNSWTL- - - - - SWTLTQDPRSP- - - - - GHFLRNIRHRLPA
hML4	175	VP- - - - - E- - - - - QDTRTLEWNSWTL- - - - - SWTLTQDPRSP- - - - - GHFLRNIRHRLPA
hML	251	PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML2	247	PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML3	226	TQ- - - - - PPAWIFSF- - - - - NPSSYWT- - - - - VYALPSS- - - - -
hML4	222	TQ- - - - - PPAWIFSF- - - - - NPSSYWT- - - - - VYALPSS- - - - -
hML	301	PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML2	297	PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML3	251	THLAHP- - - - - C- - - - - G- - - - - P- - - - - A- - - - - S- - - - -
hML4	247	THLAHP- - - - - C- - - - - G- - - - - P- - - - - A- - - - - S- - - - -

FIG. 11

FIG. 12A

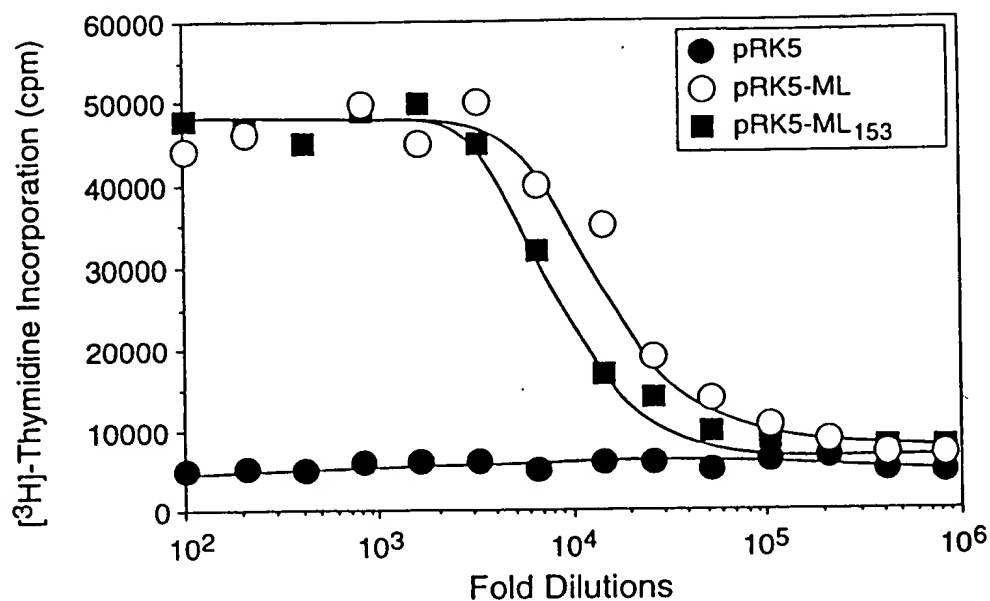


FIG. 12B

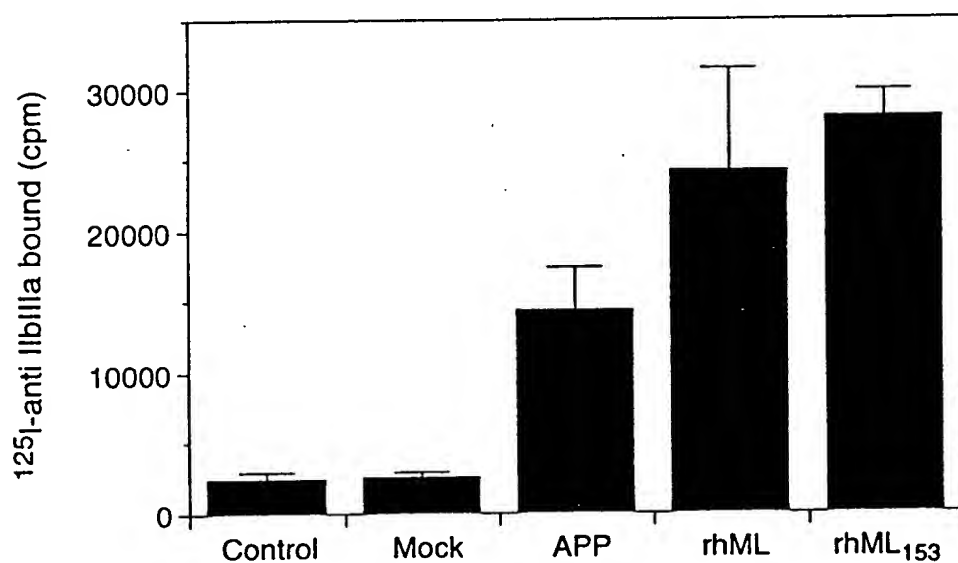
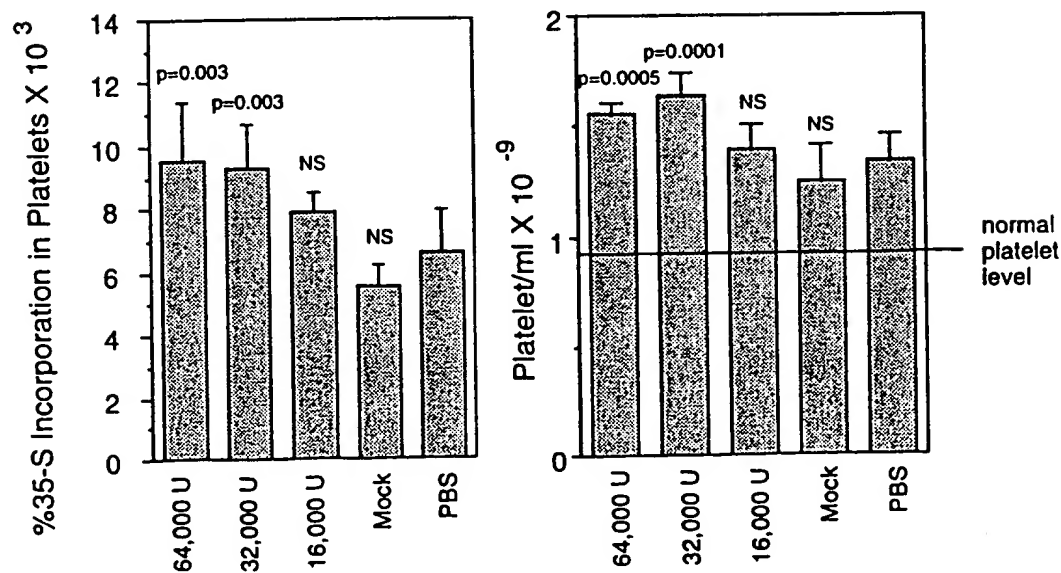


FIG. 12C



hML Proliferation Assay

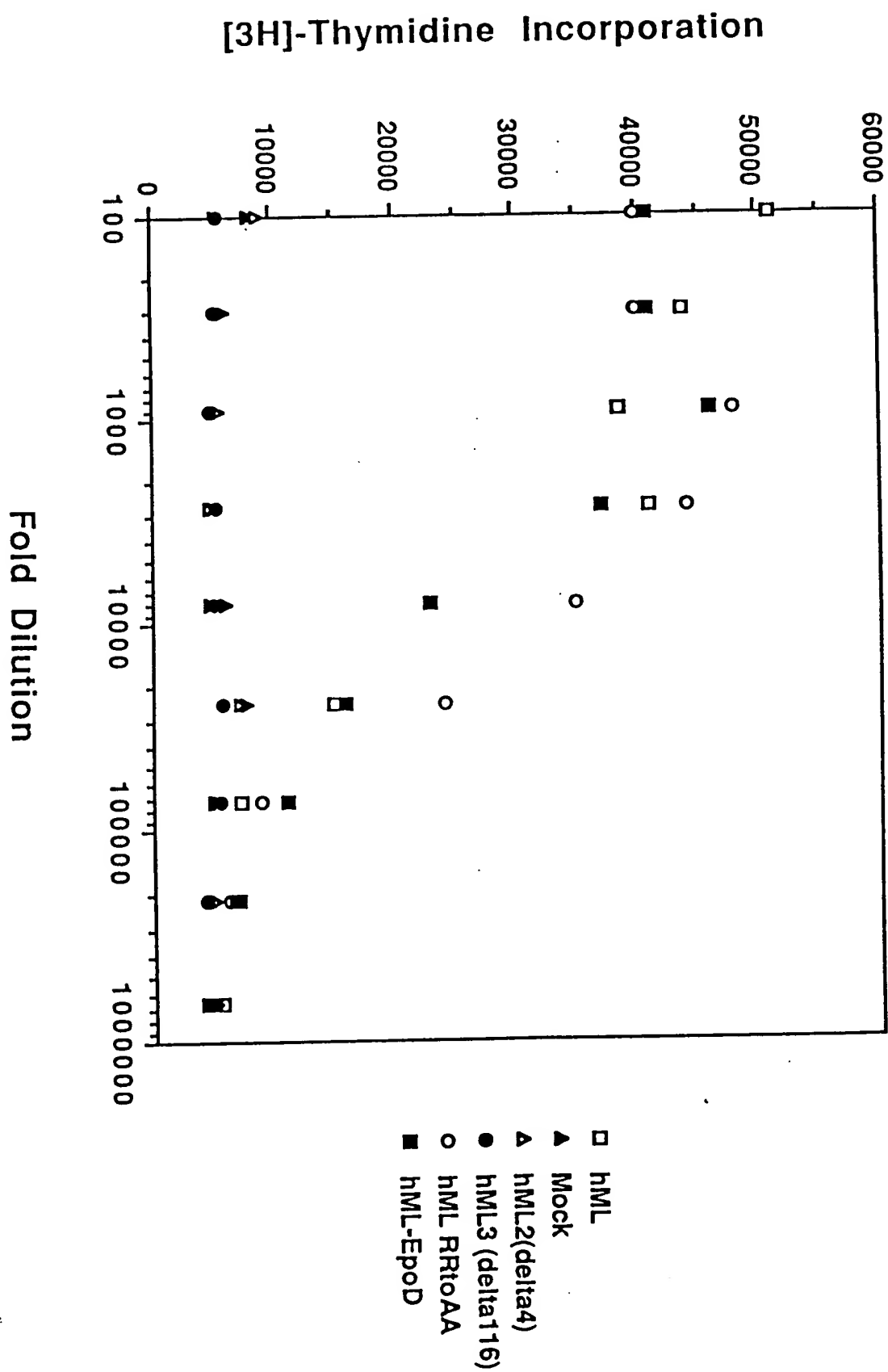


FIG. 13

1 GAGTCTCTTG CCCACCTCTC TCCACCCCA CTCTGCCGA AGAGCACAG AGCTCAAGC GCGCTCCATG GCGCCAGCA AGATTTCAGG GAGAGGCCCC
 101 ATACAGGAG CCACTTCAGT TAGACACCT GCGCAGATG GAGCTGACTG ATTCTCTCT GCGGCCATG CTCTTCGAG TCGCAGACT AACTCTGTCC
 201 SerProVala laProAlaCy sAspProArg LeuLeuasnL ysLeuLeuar gAspSerHis LeuLeuHis sArArgLeuSe rGlnCysPro AspValaspPro
 301 CTTTGTCTAT CCTCTTCTG CTGCTGCTG TCGACTTTAG CTGCGGAG TCGAATAATA AACTCTGCG TGACTGCCAG CTCTTCACA GCGCACTGAG TCGTGTCTCC GAGCTGACC
 401 LeuSeril eProValLeu LeuProAlaV alaspHeSe fLeuGlyGlu TrpLysThrG lnThrGluGl nSerLysAla GlnaspIleL euGlyAlaVal
 501 CTTTGTCTAT CCTCTTCTG CTGCTGCTG TCGACTTTAG CTGCGGAG TCGAATAATA AACTCTGCG TGACTGCCAG CTCTTCACA GCGCACTGAG TCGTGTCTCC GAGCTGACC
 601 ValArgPh eLeuLeuLeu ValGluGlyP roThrLeuCY aValArgArg ThrLeuProT hThrAlaVa lProSerSer ThrSerGlnL euLeuThrLeu
 701 AAspLysPhe ProAsnArgT hrSerGlyLe uLeuGluThr AsnPheSerV alThrAlaAr gThrAlaGly ProGlyLeuL euSerArgLe uGlnGlyPhe
 801 ArgValLysI leThrProG lYGlnLeuAsn GlnThrSerA rGsrProVa lGlnLieser GlyTyLeuA snArgThrHi sGlyProVal AsnGlyThrHis
 901 GlyLeuph eAlaGlyThr SerLeuGlnT hrLeuClua lAspAspile SerProGlyA laPheAsnLy sGlySerLeu AlaPheAsnL euGlnGlyGly
 1001 LeuProPro SerProSerL euAlaProAs pGlyHisThr ProPheProp roSerProAl aLeuProThr ThrHisGlyS erProProG lNLeuHisPro
 1101 LeuPheProA spProSerTh rThrMetPro AsnSerThrA laProHisPr oValThrMet TyrProHisP roArgAsnLe uSerGlnGlu Thr
 1201 GGCACCTGCC CAGTCAGGCT CTGACGCTTC TCTCGGCGAC AAGCTTCCCC AGGAGGCGCT GCACTCTGCT CAGATGTCTCT GCTTTCACTT
 1301 AAAAGGCGCT GCGGAGGCGA TACACAGCAC TGGAGATTGT AAATTTTAG GAGCTATTCT TTTTAACTT ATCAGCATA TTAATCAGAG CAGTACCGA
 1401 TCTTTGTGCT ATTTTCGCTA TAAATTGGA ATCACTAAT TCT

FIG. 14

hML3 1 SPAPACDLRVLSKLLRDSHV LHSRLSOCPEVHPPLPTPVLLPAVD FSLGE
mML3 1 SPVAPACDPRLLNKLLRDSHL LHSRLSOCPDVDPLSIPVLLPAVD FSLGE

hML3 51 WKTQMEETKAODILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
mML3 51 WKTQTETQSKAODILGAVSLLLEGVMAARGQLEPSCLSSLLGQLSGQVRLL

hML3 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFOHLLRGKDFWIVGDKLHCL
mML3 101 LGALQGLLGTQLPLQGRTTAHKDPNALFLSLQOLLRGKDFWIVGDELOCH

hML3 151 SONYWLWASEVAAAGIOSQD-SWSAEPNLOVPGPNPRIPEQDTRTLEWNSW
mML3 151 SONCWPWTSEQAASGIOSQDYSWSAKSNLOVPSPNLWIPEQDTRTCEWNSW

hML3 200 T LSWTLTODPRS PGHFLRNIRHRLPATQPPAWIFSFNPSSSYWTYYALPS
mML3 201 ALCWNLTSDPGSLRHRLARSFQORLPGIQPPGWTS SFSKPCS

hML3 250 STHLAHPCGPAPPPAS

FIG. 16

m-ML	1	SPVA	PACDPRL	LNKLL	RDSH	L	LHSRL	SQCP	DV	D	PLSI	IPVLL	PAVDF	SLGE																																						
p-ML	1	SPAP	PACDPRL	LNKLL	RDSH	V	LHG	RLSQCP	D	I	NPL	STPVLL	PAVDF	TLGE																																						
h-ML	1	SPAP	PACD	L	R	V	L	S	KLL	RDSH	V	LHS	R	L	SQCP	E	V	H	P	L	P	T	P	V	L	L	PAVDF	SLGE																								
m-ML	51	WKTQ	TEQ	S	K	A	Q	D	I	L	G	A	V	S	L	L	E	G	V	M	A	A	R	G	Q	L	E	P	S	C	L	S	S	L	L	G	Q	L	S	G	Q	V	R	L	L							
p-ML	51	WKTQ	TEQ	T	K	A	Q	D	V	L	G	A	T	T	L	L	E	A	V	M	T	A	R	G	Q	V	G	P	P	C	L	S	S	L	L	V	Q	L	S	G	Q	V	R	L	L							
h-ML	51	WKTQ	M	E	E	T	K	A	Q	D	I	L	G	A	V	T	L	L	E	G	V	M	A	A	R	G	Q	L	G	P	T	C	L	S	S	L	L	G	Q	L	S	G	Q	V	R	L	L					
m-ML	101	L	G	A	L	Q	S	L	L	G	T	T	Q	L	P	L	Q	G	R	T	T	A	H	K	D	P	N	A	L	F	L	S	L	Q	Q	L	L	R	G	K	V	R	F	L	L	V	E	G	P	T	L	
p-ML	101	L	G	A	L	Q	D	L	L	G	M	Q	L	P	P	Q	G	R	T	T	A	H	K	D	P	S	A	I	F	L	N	F	Q	Q	L	L	R	G	K	V	R	F	L	L	V	V	G	P	S	L		
h-ML	101	L	G	A	L	Q	S	L	L	G	T	T	Q	L	P	P	Q	G	R	T	T	A	H	K	D	P	N	A	I	F	L	S	F	Q	H	L	L	R	G	K	V	R	F	L	M	L	V	G	S	T	L	
m-ML	151	C	V	R	R	T	L	P	T	T	A	V	P	S	S	T	S	Q	L	T	L	N	K	F	P	N	R	T	S	G	L	L	E	T	N	F	S	V	T	A	R	T	A	G	P	G	L	L	S	R		
p-ML	151	C	A	K	R	A	P	P	A	I	A	V	P	S	S	T	S	P	F	H	T	L	N	K	L	P	N	R	T	S	G	L	L	E	T	N	S	I	S	A	R	T	T	G	S	G	F	L	K	R		
h-ML	151	C	V	R	R	A	P	P	T	T	A	V	P	S	R	T	S	L	V	L	T	L	N	E	L	P	N	R	T	S	G	L	L	E	T	N	F	T	I	A	S	A	R	T	T	G	S	G	L	L	K	W
m-ML	201	L	Q	G	F	R	V	K	I	T	P	G	Q	L	N	Q	T	S	R	S	P	V	Q	I	S	G	Y	L	N	R	T	H	G	P	V	N	G	T	H	G	L	F	A	G	T	S	L	Q	T	L	E	
p-ML	201	L	Q	A	F	R	A	K	I	-	P	G	L	L	N	Q	T	S	R	S	L	D	Q	I	P	G	H	Q	N	G	T	H	G	P	L	S	G	I	H	G	L	F	P	G	P	Q	P	G	A	L	G	
h-ML	201	Q	Q	G	F	R	A	K	I	-	P	G	L	L	N	Q	T	S	R	S	L	D	Q	I	P	G	Y	L	N	R	I	H	E	L	L	N	G	T	R	G	L	F	P	G	P	S	R	R	T	L	G	
m-ML	251	A	S	D	I	S	P	G	A	F	N	K	G	S	L	A	F	N	L	Q	G	G	L	P	P	S	P	S	L	A	P	D	G	H	-	T	P	F	P	P	S	P	A	L	P	T	I	H	G	S	P	
p-ML	250	A	P	D	I	P	P	A	T	S	G	M	G	S	R	P	T	Y	L	Q	P	G	E	S	P	S	P	A	H	P	S	P	G	R	Y	T	L	F	S	P	S	P	T	S	P	S	-	-	P	T		
h-ML	250	A	P	D	I	S	G	T	S	D	T	G	S	L	P	P	N	L	Q	P	G	Y	S	P	S	P	T	H	P	P	T	G	Q	Y	T	L	F	P	L	P	P	T	L	P	T	-	-	P	V			
m-ML	300	P	Q	L	H	P	L	F	P	D	P	S	T	T	M	P	N	S	T	A	P	H	P	V	T	M	Y	P	H	P	R	N	L	S	Q	E	T															
p-ML	297	V	Q	L	Q	P	L	L	P	D	P	S	A	I	T	P	N	S	T	S	P	L	L	F	A	A	H	P	H	F	Q	N	L	S	Q	E	E															
h-ML	297	V	Q	L	H	P	L	L	P	D	P	S	A	P	T	P	T	S	P	L	L	N	T	S	Y	T	H	S	Q	N	L	S	Q	E	G																	

FIG. 17

[illegible]

FIG. 18

SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro
 1 AGCCGGCTCCTCGCTGCTGACCCCCGACTCCTAAATAAACTGCTTCGTGACTCCCATGTCTTCACGGCAGACTGAGCCAGTGCCAGACATTAACC
 50
 LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr
 101 CTTTGTCCACACCTGCTCCTGCTGCTGCTGGACTTCACCTTGGGAGAAATGGAAACCCAGACGAGCAGACAAAGGCACAGGATGTCTCTGGAGCCAC
 60
 ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu
 190
 201 AACCCCTTCTGCTGGAGCAGTGATGACAGCAGCGGGACAAGTGGACCCCTTGCCTCTCATCCCTGCTGCTGGTGCAGCTTTCTGGACAGGTTCCCTTCCTC
 130
 LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeuLeuArgGlyLys
 301 CTCGGGGCCCTGCAGGACCTCCTTTGGAATGCAGGAAGGACCACAGCTCACAAAGGATCCAGTGCCATCTTCTCTGAACCTTCCAAACAACACTGCTCCGAGGAA
 160
 ValArgPheLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerProPheHisThrLeu
 401 AGGTGCGTTTCTGCTCCTTGTAGTGGGSCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCATAGCTGTCCCGAGCAGCACCTCTCCATTCACACACT
 150
 AsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArgLeuGlnAlaPhe
 180
 501 GAACAAGCTCCCAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGGCTGCAGGCATTCTC
 200
 ArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSerGlyIleHisGly
 220
 601 AGAGCCAAGATTCTGGTCTGCTGTAACCAACCTCCAGGTCCCTAGACCAGTCCCTAGACCAATCCCTGGACACCAGAAATGGGACACACACGACCCCTTGAGTGGAAATTCATG
 240
 LeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrThrLeuGlnProGlyGlu
 701 GACTCTTTCTTGACCCCAACCCGGGCCCTCGGAGCTCCAGACATTCTCCAGCAACTTCAGGCATGGGTCCCCGGCCCAACCTACCTCCAGCCTGGAGA
 260
 SerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGlnProLeuLeuPro
 280
 801 GTCTCTTCCCCAGCTCACCCCTTCTCCTGGACGATACACTCTCTCTCTCTCCTTACCCACCTCGCCCCCTCCCCACAGTCCAGCTCCAGCCTTGCTTCCT
 300
 AspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
 320
 901 GACCCCTCTGGGATCACACCCAACTCTACCGAGTCTTCTATTGTCAGCTCACCCCTCATTTCCAGAACCTGTCTTCAGGAAGAGTAAGGTGCTCAGACCC
 340
 001 TGCCAACTTCAGCA

FIG. 19

pML	1	SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE	
pML2	1	SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE	
pML	51	WKTQTEOTKAODVLGATTLLLEAVMTARGOVGPPCLSSLLVQLSGOVRLL	
pML2	51	WKTQTEOTKAODVLGATTLLLEAVMTARGOVGPPCLSSLLVQLSGOVRLL	
pML	101	LGALODLLGM	OLPP
pML2	101	LGALODLLGM	OGRTTAHKDPSAIFLNFOQLLRGKVRFLLLTVGPSL
pML	151	CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR	
pML2	147	CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR	
pML	201	LQAFRAKIPGLLNOTSRSLEOIPGHONGTHGPLSGIHGLFPGPOPGALGA	
pML2	197	LQAFRAKIPGLLNOTSRSLEOIPGHONGTHGPLSGIHGLFPGPOPGALGA	
pML	251	PDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSPTVQLQ	
pML2	247	PDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSPTVQLQ	
pML	301	PLLPDPSAITPNSTSPLLFAAHPHFQNLSEEE	
pML2	297	PLLPDPSAITPNSTSPLLFAAHPHFQNLSEEE	

FIG. 20